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EXAMINER	
GANGLE, BRIAN J	

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1645	

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Please find below and/or attached an Office communication concerning this application or proceeding.

The time period for reply, if any, is set in the attached communication.

Office Action Summary	Application No.	Applicant(s)	
	10/594,461	ESCAICH, SONIA	
	Examiner	Art Unit	
	Brian J. Gangle	1645	

-- The MAILING DATE of this communication appears on the cover sheet with the correspondence address --

Period for Reply

A SHORTENED STATUTORY PERIOD FOR REPLY IS SET TO EXPIRE *3* MONTH(S) OR THIRTY (30) DAYS, WHICHEVER IS LONGER, FROM THE MAILING DATE OF THIS COMMUNICATION.

- Extensions of time may be available under the provisions of 37 CFR 1.136(a). In no event, however, may a reply be timely filed after SIX (6) MONTHS from the mailing date of this communication.
- If NO period for reply is specified above, the maximum statutory period will apply and will expire SIX (6) MONTHS from the mailing date of this communication.
- Failure to reply within the set or extended period for reply will, by statute, cause the application to become ABANDONED (35 U.S.C. § 133). Any reply received by the Office later than three months after the mailing date of this communication, even if timely filed, may reduce any earned patent term adjustment. See 37 CFR 1.704(b).

Status

1)☒ Responsive to communication(s) filed on *04 November 2009*.

2a)☐ This action is **FINAL**. 2b)☒ This action is non-final.

3)☐ Since this application is in condition for allowance except for formal matters, prosecution as to the merits is closed in accordance with the practice under *Ex parte Quayle*, 1935 C.D. 11, 453 O.G. 213.

Disposition of Claims

4)☒ Claim(s) *1-28* is/are pending in the application.

4a) Of the above claim(s) *3,5,7-19 and 21-27* is/are withdrawn from consideration.

5)☐ Claim(s) _____ is/are allowed.

6)☒ Claim(s) *1,2,4,6,20 and 28* is/are rejected.

7)☐ Claim(s) _____ is/are objected to.

8)☐ Claim(s) _____ are subject to restriction and/or election requirement.

Application Papers

9)☒ The specification is objected to by the Examiner.

10)☒ The drawing(s) filed on *26 September 2006* is/are: a)☒ accepted or b)☐ objected to by the Examiner.

Applicant may not request that any objection to the drawing(s) be held in abeyance. See 37 CFR 1.85(a).

Replacement drawing sheet(s) including the correction is required if the drawing(s) is objected to. See 37 CFR 1.121(d).

11)☐ The oath or declaration is objected to by the Examiner. Note the attached Office Action or form PTO-152.

Priority under 35 U.S.C. § 119

12)☐ Acknowledgment is made of a claim for foreign priority under 35 U.S.C. § 119(a)-(d) or (f).

a)☐ All b)☐ Some * c)☐ None of:

1.☐ Certified copies of the priority documents have been received.

2.☐ Certified copies of the priority documents have been received in Application No. _____.

3.☐ Copies of the certified copies of the priority documents have been received in this National Stage application from the International Bureau (PCT Rule 17.2(a)).

* See the attached detailed Office action for a list of the certified copies not received.

Attachment(s)

1) ☒ Notice of References Cited (PTO-892)
2) ☐ Notice of Draftsperson's Patent Drawing Review (PTO-948)
3) ☒ Information Disclosure Statement(s) (PTO/SB/08) Paper No(s)/Mail Date *9/26/2006*.
4) ☐ Interview Summary (PTO-413) Paper No(s)/Mail Date. _____ .
5) ☐ Notice of Informal Patent Application
6) ☐ Other: _____.

DETAILED ACTION

Election/Restrictions

Applicant's election of Group I and the combination of SEQ ID NO:145 and 159 in the reply filed on 11/4/2009 is acknowledged. Because applicant did not distinctly and specifically point out the supposed errors in the restriction requirement, the election has been treated as an election without traverse (MPEP § 818.03(a)).

It is noted that applicant has referred to the election of the combination of SEQ ID NO:145 and 159 as a species election. As set forth in the restriction requirement of 8/4/2009, the sequence election was not a species election. Each combination of sequences is a separate invention since there is no special technical feature shared by the different combinations. These combinations were not listed because it was not feasible to list the thousands of possible combinations encompassed by the claims.

Claims 1-28 are pending. Claims 3, 5, 7-19, and 21-27 are withdrawn as being drawn to nonelected invention. Claims 1-2, 4, 6, 20, and 28 are currently under examination.

Information Disclosure Statement

The information disclosure statement filed on 9/26/2006 has been considered. An initialed copy is enclosed.

Specification

The disclosure is objected to because of the following informalities: The specification makes reference, in numerous places to "SEQ ID N°". Sequences are correctly identified by the phrase "SEQ ID NO".

Appropriate correction is required.

Claim Objections

Claims 1, 2, 4, 6, and 20 are objected to because of the following informalities: The claims refer to sequences by "SEQ ID N°". Sequences are correctly identified by the phrase "SEQ ID NO".

Claim 4 is objected to because of the following informalities: The phrase "combination of two polypeptides comprises polypeptide having sequence SEQ ID N°" is grammatically incorrect. When using plural nouns, the verb form should agree (i.e., two polypeptides *comprise*). Further, "having sequence SEQ ID" should read "having the sequence of SEQ ID."

Claim 20 is objected to because of the following informalities: In scientific nomenclature, genus and species names are italicized.

Claim 28 is objected to because of the following informalities: In scientific nomenclature, genus names are capitalized and species names are not.

Appropriate correction is required.

Claim Rejections - 35 USC § 101

35 U.S.C. 101 reads as follows:

> Whoever invents or discovers any new and useful process, machine, manufacture, or composition of matter, or any new and useful improvement thereof, may obtain a patent therefor, subject to the conditions and requirements of this title.

Claims 1-2 and 4 are rejected under 35 U.S.C. 101 because the claimed invention is directed to non-statutory subject matter. Products of nature are not patentable because they do not reflect the "hand of man" in the production of the product or manufacturing process. Diamond v. Chakrabarty, 206 USPQ 193 (1980). The specification describes the claimed polypeptides as natural proteins produced by *E. coli*. As the claims lack any recitation of an isolated polypeptide, they encompass natural *E. coli* cells.

Claim Rejections - 35 USC § 112

The following is a quotation of the first paragraph of 35 U.S.C. 112:

> The specification shall contain a written description of the invention, and of the manner and process of making and using it, in such full, clear, concise, and exact terms as to enable any person skilled in the art to which it pertains, or with which it is most nearly connected, to make and use the same and shall set forth the best mode contemplated by the inventor of carrying out his invention.

Claims 1-2, 6, 20, and 28 are rejected under 35 U.S.C. 112, first paragraph, as failing to comply with the written description requirement. The claim(s) contains subject matter which was not described in the specification in such a way as to reasonably convey to one skilled in the

relevant art that the inventor(s), at the time the application was filed, had possession of the claimed invention.

Claims 1-2, 6, and 28 are drawn to compositions of polypeptides specific to pathogenic strains comprising polypeptides of a first group and of a second group, having 25% homology to specific sequences (the elected sequences are 145 and 159). For claim 28, the composition is for alleviating and/or preventing and/or treating an undesirable growth of *E. coli*.

Claim 20 is drawn to vaccine compositions specific to *E. coli* extraintestinal infection, comprising an effective amount of at least one antigenic polypeptide or fragment thereof and at least one antigenic polypeptide or fragment thereof of the second group, with a carrier, particularly, SEQ ID NO:145 or homologous polypeptides and SEQ ID NO:159 or homologous polypeptides.

The specification discloses specific sequences from B2/D *E. coli* which is an *E. coli* ExPEC strain. ExPEC strains are those which can be part of the normal gastrointestinal flora of humans and which are often responsible for extra-intestinal infections such as urinary tract infections. Combinations of SEQ ID NO:159+145, 159+2, and 159+34 were shown to protect mice from death in a challenge experiment using a B2 strain of *E. coli*.

However, claims 1-2, 6, and 28 encompass polypeptides with as little as 25% homology with SEQ ID NO:145 and 159 and claim 20 encompass any antigenic polypeptide or fragment thereof. Claim 20 is not limited even to homologues of SEQ ID NO:145 and 159, and even where it states that these are preferred, there is no recitation of any particular degree of homology.

These peptides have no correlation between their structure and the functions required by the claims. The peptides of claims 1-2, 6, and 28 must be specific to pathogenic strains. There is no disclosure of which of the peptides encompassed by the claims have this specificity and there is no correlation, either in the art or the specification, that shows how any particular homology to SEQ ID NO:145 or 159 would make a peptide specific to a pathogenic strain. The vaccine of claim 20 must be specific to *E. coli* extraintestinal infections. According to the specification, *E. coli* strains can be generally classified into commensal, intestinal pathogenic, and extra-intestinal pathogenic strains. While commensal and intestinal strains do not *generally* cause extra-intestinal disease, these strains *are* capable of causing disease outside the intestinal tract,

especially when there are precipitating factors present, such as an indwelling foreign body or impairment of host defenses (Russo *et al.*, J. Infect. Dis., 181:1753-1754). The specification shows that extra-intestinal strains are responsible for the majority of extra-intestinal infections, and suggests that there are immunogenic markers specific to these strains. However, applicant has not described any means of producing a vaccine which is specific to all extra-intestinal *E. coli* infections. Even if the claimed composition (which encompasses any antigenic polypeptides) were shown to be specific and protective against extra-intestinal strains of *E. coli* (which is has not), this polypeptide would not provide specific protection from all extra-intestinal infections caused by *E. coli*. Such a vaccine would provide no protection from strains other than so-called ExPEC *E. coli* strains, even though "commensal" and "intestinal" strains could cause extra-intestinal disease. Furthermore, claim 28 is not limited to treatments in humans or animals. The claim encompasses treating or preventing any undesirable growth of *E. coli*. Since applicant's claims are directed toward polypeptides (which might or might not induce an appropriate immune response), one of skill in the art would have no expectation that administering an antigenic polypeptide, or fragment thereof, would in any way alter growth of *E. coli* in food or on surfaces.

The specification provides no guidance regarding which of the polypeptides encompassed by the claims are capable of the required function. Therefore, the specification provides insufficient written description to support the genus encompassed by the claim. Vas-Cath Inc. v. Mahurkar, 19 USPQ2d 1111, makes clear that

"applicant must convey with reasonable clarity to those skilled in the art that, as of the filing date sought, he or she was in possession of the invention. The invention is, for purposes of the 'written description' inquiry, whatever is now claimed." (See page 1117.) The specification does not "clearly allow persons of ordinary skill in the art to recognize that [he or she] invented what is claimed." (See Vas-Cath at page 1116.)

With the exception of the combination of SEQ ID NO:145 and 159 (and then only for limited uses), the skilled artisan cannot envision the detailed chemical structure of the encompassed polypeptides, regardless of the complexity or simplicity of the method of isolation. Adequate written description requires more than a mere statement that it is part of the invention and reference to a potential method for isolating it. The nucleic acid and/or protein itself is required. See Fiers v. Revel, 25 USPQ2d 1601, 1606 (CAFC 1993) and Amgen Inc. V. Chugai

Pharmaceutical Co. Ltd., 18 USPQ2d 1016. In Fiddes v. Baird, 30 USPQ2d 1481, 1483, claims directed to mammalian FGF's were found unpatentable due to lack of written description for the broad class. The specification provided only the bovine sequence.

University of California v. Eli Lilly and Co., 43 USPQ2d 1398, 1404. 1405 held that:

...To fulfill the written description requirement, a patent specification must describe an invention and does so in sufficient detail that one skilled in the art can clearly conclude that "the inventor invented the claimed invention." Lockwood v. American Airlines Inc. , 107 F.3d 1565, 1572, 41 USPQ2d 1961, 1966 (1997); In re Gosteli , 872 F.2d 1008, 1012, 10 USPQ2d 1614, 1618 (Fed. Cir. 1989) (" [T]he description must clearly allow persons of ordinary skill in the art to recognize that [the inventor] invented what is claimed."). Thus, an applicant complies with the written description requirement "by describing the invention, with all its claimed limitations, not that which makes it obvious," and by using "such descriptive means as words, structures, figures, diagrams, formulas, etc., that set forth the claimed invention." Lockwood, 107 F.3d at 1572, 41 USPQ2datl966.

Protein chemistry is probably one of the most unpredictable areas of biotechnology. Consequently, the effects of sequence dissimilarities upon protein structure and function cannot be predicted. Bowie *et al.* (Science, 1990, 247:1306-1310) teach that an amino acid sequence encodes a message that determines the shape and function of a protein and that it is the ability of these proteins to fold into unique three-dimensional structures that allows them to function and carry out the instructions of the genome and further teaches that the problem of predicting protein structure from sequence data and in turn utilizing predicted structural determinations to ascertain functional aspects of the protein is extremely complex (column 1, page 1306). Bowie *et al.* further teach that while it is known that many amino acid substitutions are possible in any given protein, the position within the protein's sequence where such amino acid substitutions can be made with a reasonable expectation of maintaining function are limited. Certain positions in the sequence are critical to the three dimensional structure/function relationship and these regions can tolerate only conservative substitutions or no substitutions at all (column 2, page 1306). The sensitivity of proteins to alterations of even a single amino acid in a sequence are exemplified by Burgess *et al.* (J. Cell Biol. 111:2129-2138, 1990) who teach that replacement of a single lysine reside at position 118 of acidic fibroblast growth factor by glutamic acid led to the substantial loss of heparin binding, receptor binding and biological activity of the protein and by Lazar *et al.* (Mol. Cell. Biol., 8:1247-1252, 1988) who teach that in transforming growth factor

alpha, replacement of aspartic acid at position 47 with alanine or asparagine did not affect biological activity while replacement with serine or glutamic acid sharply reduced the biological activity of the mitogen. These references demonstrate that even a single amino acid substitution will often dramatically affect the biological activity and characteristics of a protein. Additionally, Bork (Genome Research, 2000,10:398-400) clearly teaches the pitfalls associated with comparative sequence analysis for predicting protein function because of the known error margins for high-throughput computational methods. Bork specifically teaches that computational sequence analysis is far from perfect, despite the fact that sequencing itself is highly automated and accurate (p. 398, column 1). One of the reasons for the inaccuracy is that the quality of data in public sequence databases is still insufficient. This is particularly true for data on protein function. Protein function is context dependent, and both molecular and cellular aspects have to be considered (p. 398, column 2). Conclusions from the comparison analysis are often stretched with regard to protein products (p. 398, column 3). Further, although gene annotation via sequence database searches is already a routine job, even here the error rate is considerable (p. 399, column 2). Most features predicted with an accuracy of greater than 70% are of structural nature and, at best, only indirectly imply a certain functionality (see legend for table 1, page 399). As more sequences are added and as errors accumulate and propagate it becomes more difficult to infer correct function from the many possibilities revealed by database search (p. 399, paragraph bridging columns 2 and 3). The reference finally cautions that although the current methods seem to capture important features and explain general trends, 30% of those features are missing or predicted wrongly. This has to be kept in mind when processing the results further (p. 400, paragraph bridging cols 1 and 2). Given not only the teachings of Bowie *et al.*, Lazar *et al.* and Burgess *et al.* but also the limitations and pitfalls of using computational sequence analysis and the unknown effects of alternative splicing, post translational modification and cellular context on protein function as taught by Bork, the function of the claimed proteins could not be predicted based on sequence identity to SEQ ID NO:145 and 159. Clearly, it could not be predicted that a polypeptide or a variant that shares only partial homology with a disclosed protein will function in a given manner.

Therefore, only the composition with the combination of SEQ ID NO:145 and 159, but not the full breadth of the claims, meet the written description provision of 35 USC 112, first

paragraph for claims 1-2 and 6. Claims 20 and 28 do not meet the written description requirements. The species specifically disclosed are not representative of the genus because the genus is highly variant. Applicant is reminded that Vas-Cath makes clear that the written description provision of 35 USC 112 is severable from its enablement provision. (See page 1115).

Claims 20 and 28 are rejected under 35 U.S.C. 112, first paragraph, as failing to comply with the enablement requirement. The claim(s) contains subject matter which was not described in the specification in such a way as to enable one skilled in the art to which it pertains, or with which it is most nearly connected, to make and/or use the invention.

Enablement is considered in view of the Wands factors (MPEP 2164.01(A)). These include: nature of the invention, breadth of the claims, guidance of the specification, the existence of working examples, state of the art, predictability of the art and the amount of experimentation necessary.

In re Fisher, 427 F.2d 833, 839, 166 USPQ 18, 24 (CCPA 1970) states, "The amount of guidance or direction needed to enable the invention is inversely related to the amount of knowledge in the state of the art as well as the predictability in the art." "The "amount of guidance or direction" refers to that information in the application, as originally filed, that teaches exactly how to make or use the invention. The more that is known in the prior art about the nature of the invention, how to make, and how to use the invention, and the more predictable the art is, the less information needs to be explicitly stated in the specification. In contrast, if little is known in the prior art about the nature of the invention and the art is unpredictable, the specification would need more detail as to how to make and use the invention in order to be enabling" (MPEP 2164.03). The MPEP further states that physiological activity can be considered inherently unpredictable. Thus, Applicant assumes a certain burden in establishing that inventions involving physiological activity are enabled. All of the Wands factors have been considered with regard to the instant claims, with the most relevant factors discussed below.

Nature of the invention: Claim 28 is drawn to compositions of polypeptides specific to pathogenic strains comprising polypeptides of a first group and of a second group, having 25%

homology to specific sequences (the elected sequences are 145 and 159), wherein the composition is for alleviating and/or preventing and/or treating an undesirable growth of *E. coli*.

Claim 20 is drawn to vaccine compositions specific to *E. coli* extraintestinal infection, comprising an effective amount of at least one antigenic polypeptide or fragment thereof and at least one antigenic polypeptide or fragment thereof of the second group, with a carrier, particularly, SEQ ID NO:145 or homologous polypeptides and SEQ ID NO:159 or homologous polypeptides.

Breadth of the claims: Claim 20 encompasses any antigenic polypeptide or fragment thereof. Claim 20 is not limited even to homologues of SEQ ID NO:145 and 159, and even where it states that these are preferred, there is no recitation of any particular degree of homology. The claimed composition must induce protective immunity specific to *E. coli* extraintestinal infections.

Claim 28 encompasses polypeptides with as little as 25% homology with SEQ ID NO:145 and 159, and the composition must alleviate and/or prevent and/or treat any undesirable growth of *E. coli*. This includes growth of all strains of *E. coli* (not just ExPEC or B2 strains) and undesirable growth in any location, including food, or surfaces such as toilets or countertops.

Guidance of the specification/The existence of working examples: The specification discloses specific sequences from B2/D *E. coli* which is an *E. coli* ExPEC strain. ExPEC strains are those which can be part of the normal gastrointestinal flora of humans and which are often responsible for extra-intestinal infections such as urinary tract infections. Combinations of SEQ ID NO:159+145, 159+2, and 159+34 were shown to protect mice from death in a challenge experiment using a B2 strain of *E. coli*.

State of the art: While the skill in the art of immunology is high, to date, prediction of a specific immune response for any given composition in any given animal is quite unpredictable. Moreover, protein chemistry is probably one of the most unpredictable areas of biotechnology. Consequently, the effects of sequence dissimilarities upon protein structure and function cannot be predicted. Bowie *et al.* (Science, 1990, 247:1306-1310) teach that an amino acid sequence encodes a message that determines the shape and function of a protein and that it is the ability of these proteins to fold into unique three-dimensional structures that allows them to function, carry out the instructions of the genome and form immunoepitopes. Bowie *et al.* further teach that the

problem of predicting protein structure from sequence data and in turn utilizing predicted structural determinations to ascertain functional aspects of the protein is extremely complex (column 1, page 1306). Bowie *et al.* further teach that while it is known that many amino acid substitutions are possible in any given protein, the position within the protein's sequence where such amino acid substitutions can be made with a reasonable expectation of maintaining function are limited. Certain positions in the sequence are critical to the three dimensional structure/function relationship and these regions can tolerate only conservative substitutions or no substitutions (column 2, page 1306). Additionally, as evidenced by Greenspan *et al.* (*Nature Biotechnology* **7**: 936-937, 1999), defining epitopes is not as easy as it seems. Greenspan *et al.* recommends defining an epitope by the structural characterization of the molecular interface between the antigen and the antibody is necessary to define an "epitope" (page 937, column 2). According to Greenspan *et al.*, an epitope will include residues that make contacts with a ligand, here the antibody, but are energetically neutral, or even destabilizing to binding. Furthermore, an epitope will not include any residue not contacted by the antibody, even though substitution of such a residue might profoundly affect binding. Accordingly, it follows that the immunoepitopes that can elicit a protective immune response to a given pathogen can only be identified empirically. Applicant has claimed a vaccine that is specific to *E. coli* extraintestinal infections. *E. coli* strains can be generally classified into commensal, intestinal pathogenic, and extra-intestinal pathogenic strains. While commensal and intestinal strains do not generally cause extra-intestinal disease, these strains are capable of causing disease outside the intestinal tract, especially when there are precipitating factors present, such as an indwelling foreign body or impairment of host defenses (Russo *et al.*, J. Infect. Dis., 181:1753-1754). The specification shows that extra-intestinal strains are responsible for the majority of extra-intestinal infections, and suggests that there are immunogenic markers specific to these strains. However, applicant has provided no means of producing a vaccine which is specific to all extra-intestinal *E. coli* infections. Even if the claimed combination of polypeptides (SEQ ID NO:145 and 159) were shown to be specific and protective against extra-intestinal strains of *E. coli* (which is has not), this polypeptide would not provide specific protection from all extra-intestinal infections caused by *E. coli*. Such a vaccine would provide no protection from strains other than extra-intestinal *E.*

coli strains, even though "commensal" and "intestinal" strains could cause extra-intestinal disease.

Furthermore, claim 28 is not limited to treatments in humans or animals. The claim encompasses treating or preventing any undesirable growth of *E. coli*. Since applicant's claims are directed toward polypeptides (which might or might not induce an appropriate immune response), one of skill in the art would have no expectation that administering an antigenic polypeptide, or fragment thereof, would in any way alter growth of *E. coli* in food or on surfaces.

Therefore, given the teachings of the art and the lack of working examples commensurate in scope to the claimed invention and the unpredictability of the generation of protective immunity, the specification, as filed, does not provide enablement for the claims as drawn. Hence, the specification is not enabling.

The following is a quotation of the second paragraph of 35 U.S.C. 112:

> The specification shall conclude with one or more claims particularly pointing out and distinctly claiming the subject matter which the applicant regards as his invention.

Claims 1-2, 4, 6, 20, and 28 are rejected under 35 U.S.C. 112, second paragraph, as being indefinite for failing to particularly point out and distinctly claim the subject matter which applicant regards as the invention.

Claim 1 is rendered vague and indefinite by the phrase "selected in the group comprising the sequences of." This is improper Markush language. Alternative expressions are permitted if they present no uncertainty or ambiguity with respect to the question of scope or clarity of the claims. One acceptable form of alternative expression, which is commonly referred to as a Markush group, recites members as being "selected from the group consisting of A, B and C." See Ex parte Markush, 1925 C.d. 126 (Comm'r Pat. 1925). It is not clear what the members of the group are due to the use of the word "comprising." In addition, the use of the word "in" is grammatically incorrect. The phrase should be "selected from the group."

Claim 1 is rendered vague and indefinite by the phrase "or homologous sequences of polypeptides of the first group and/or the second group." The sentence structure and use of commas make it unclear what is required in the composition. It appears that the choices are: a composition with (1) at least one polypeptide from the first group and at least one from a second

group; or (2) homologous sequences of polypeptides from the first group; or (3) homologous sequences of polypeptides from the second group; or (4) sequences of polypeptides from the first group and homologous sequences of polypeptides from the second group. However, it may also be that the composition is: at least one polypeptide from the first group and at least one from a second group, wherein the polypeptide from the first group is a sequence selected from SEQ ID NO:1-66 or 133-145, or homologous sequences, and the polypeptide from the second group is SEQ ID NO:159 or a homologous sequence.

Claim 4 is rendered vague and indefinite by the phrase "selected in the group comprising peptides having sequences." This is improper Markush language. Alternative expressions are permitted if they present no uncertainty or ambiguity with respect to the question of scope or clarity of the claims. One acceptable form of alternative expression, which is commonly referred to as a Markush group, recites members as being "selected from the group consisting of A, B and C." See Ex parte Markush, 1925 C.d. 126 (Comm'r Pat. 1925). It is not clear what the members of the group are due to the use of the word "comprising." In addition, the use of the word "in" is grammatically incorrect. The phrase should be "selected from the group."

Claim 4 recites the limitation "the combination of two polypeptides" in lines 1-2. There is insufficient antecedent basis for this limitation in the claim.

Claim 6 recites the limitation "said homologous isolated antigenic polypeptides" in line 2. There is insufficient antecedent basis for this limitation in the claim.

Claim 20 recites the limitation "said first group" in line 3. There is insufficient antecedent basis for this limitation in the claim.

Claim 20 recites the limitation "the second group" in lines 3-4. There is insufficient antecedent basis for this limitation in the claim.

Regarding claim 20, the phrase "particularly" renders the claim indefinite because it is unclear whether the limitations following the phrase are part of the claimed invention. See MPEP § 2173.05(d).

Claim 20 is rendered vague and indefinite by the phrases "homologous polypeptides" and "homologous peptides." The term homologous is unclear. Neither the claim nor the specification defines what type of homology is being referred to. This could be functional homology, phylogenetic homology, or morphological homology, and it is not clear how one

could measure these types of homology in terms of a percentage.

Claim Rejections - 35 USC § 102

The following is a quotation of the appropriate paragraphs of 35 U.S.C. 102 that form the basis for the rejections under this section made in this Office action:

> A person shall be entitled to a patent unless –
>
> (b) the invention was patented or described in a printed publication in this or a foreign country or in public use or on sale in this country, more than one year prior to the date of application for patent in the United States.

Claims 1-2, 4, 6, 20, and 28 are rejected under 35 U.S.C. 102(b) as being anticipated by Escaich (WO03/074553, 9/2003, IDS filed 9/26/2006).

The instant claims are drawn to compositions of polypeptides specific to pathogenic strains comprising SEQ ID NO:145 and SEQ ID NO:159.

Escaich discloses pharmaceutical compositions for alleviating and/or preventing and/or treating an undesirable growth of *E. coli* comprising an effective amount of at least one polypeptide "particularly having SEQ ID N°1-66 to 133-145," in combination with a pharmaceutically acceptable carrier (see page 13, lines 6-12). The instant SEQ ID NO:145 matches SEQ ID NO:145 of Escaich and the instant SEQ ID NO:159 matches SEQ ID NO:8 of Escaich. By using the term "at least," Escaich has expressly disclosed compositions including more than one polypeptide. Because of this, the reference discloses all combinations of SEQ ID NOs 1-66 and 133-145. Included in this is the combination of SEQ ID NO:8 and 145.

Conclusion

No claim is allowed.

Any inquiry concerning this communication or earlier communications from the examiner should be directed to Brian J. Gangle whose telephone number is (571)272-1181. The examiner can normally be reached on M-F 7-3:30.

If attempts to reach the examiner by telephone are unsuccessful, the examiner's supervisor, Robert Mondesi can be reached on 571-272-0956. The fax phone number for the organization where this application or proceeding is assigned is 571-273-8300.

Information regarding the status of an application may be obtained from the Patent Application Information Retrieval (PAIR) system. Status information for published applications may be obtained from either Private PAIR or Public PAIR. Status information for unpublished applications is available through Private PAIR only. For more information about the PAIR system, see http://pair-direct.uspto.gov. Should you have questions on access to the Private PAIR system, contact the Electronic Business Center (EBC) at 866-217-9197 (toll-free). If you would like assistance from a USPTO Customer Service Representative or access to the automated information system, call 800-786-9199 (IN USA OR CANADA) or 571-272-1000.

/Brian J Gangle/
Examiner, Art Unit 1645

/Robert B Mondesi/
Supervisory Patent Examiner,
Art Unit 1645